



Clustering of respiratory symptoms in the general population

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Aim

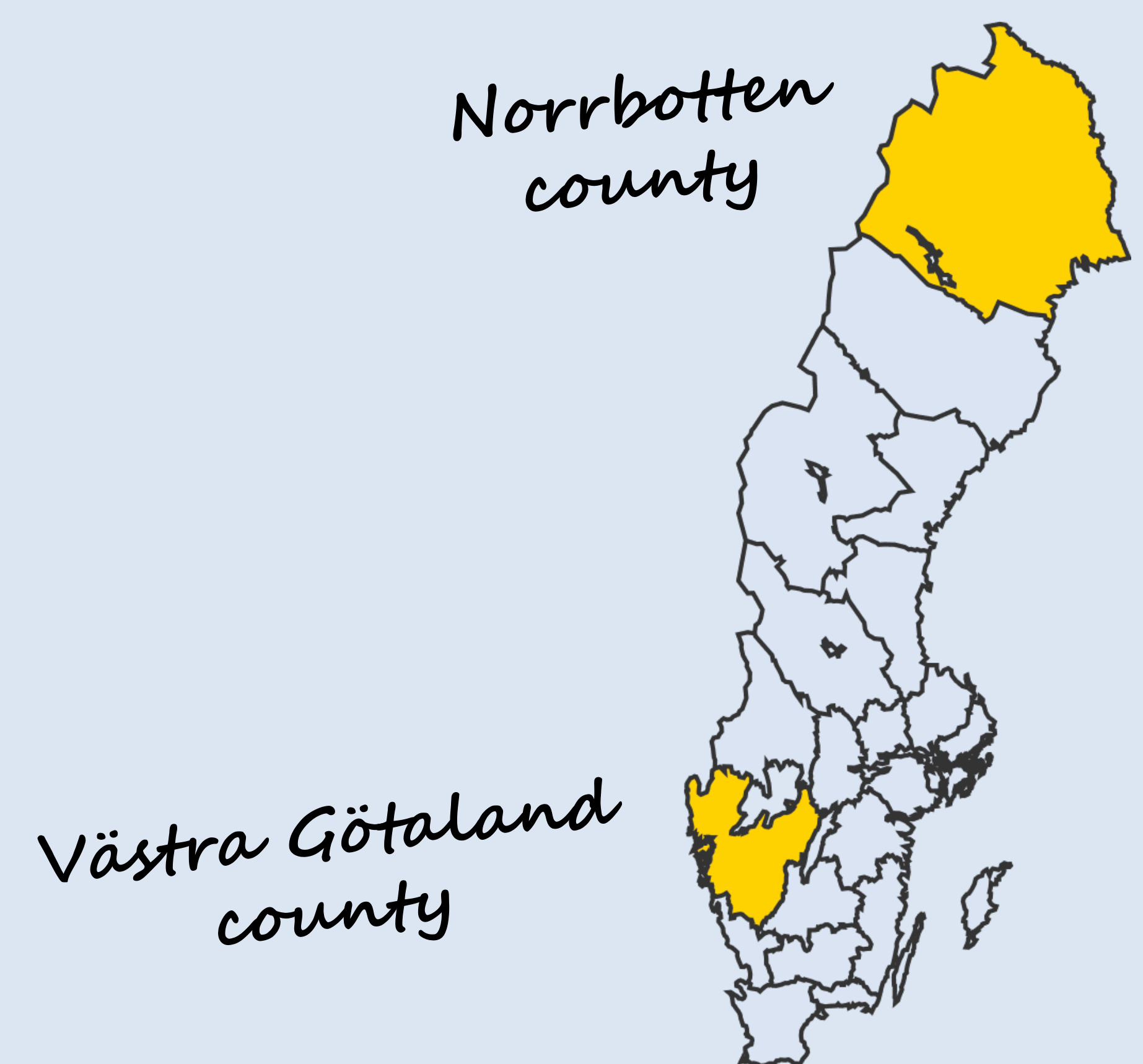
To perform computational phenotyping of respiratory symptoms in a population-representative selection of adults.

Methods

Survey data on respiratory health/symptoms were gathered from population-based cohorts in Northern and Western Sweden. The initial selection of 50 variables was reduced to 10 using principal component analysis (PCA). Four algorithms (K-means, deep embedded clustering (DEC), Dip-based deep embedded clustering (DipDeck), and Kingdra) were used for clustering. Internal validation was assessed with Silhouette score.

Results

The study population consisted of 61,530 adults. The strongest clusters were found using K=5 with DEC. Cluster 1: asthma with few symptoms, history of asthma/allergy; cluster 2: late-diagnosed asthma, more (particularly nightly) symptoms; cluster 3: respiratory symptoms from exercise/tobacco smoke, fatigue; cluster 4: middle-age, few respiratory symptoms and comorbidities; cluster 5: senior age, few respiratory symptoms, common comorbidities of age (e.g., hypertension).



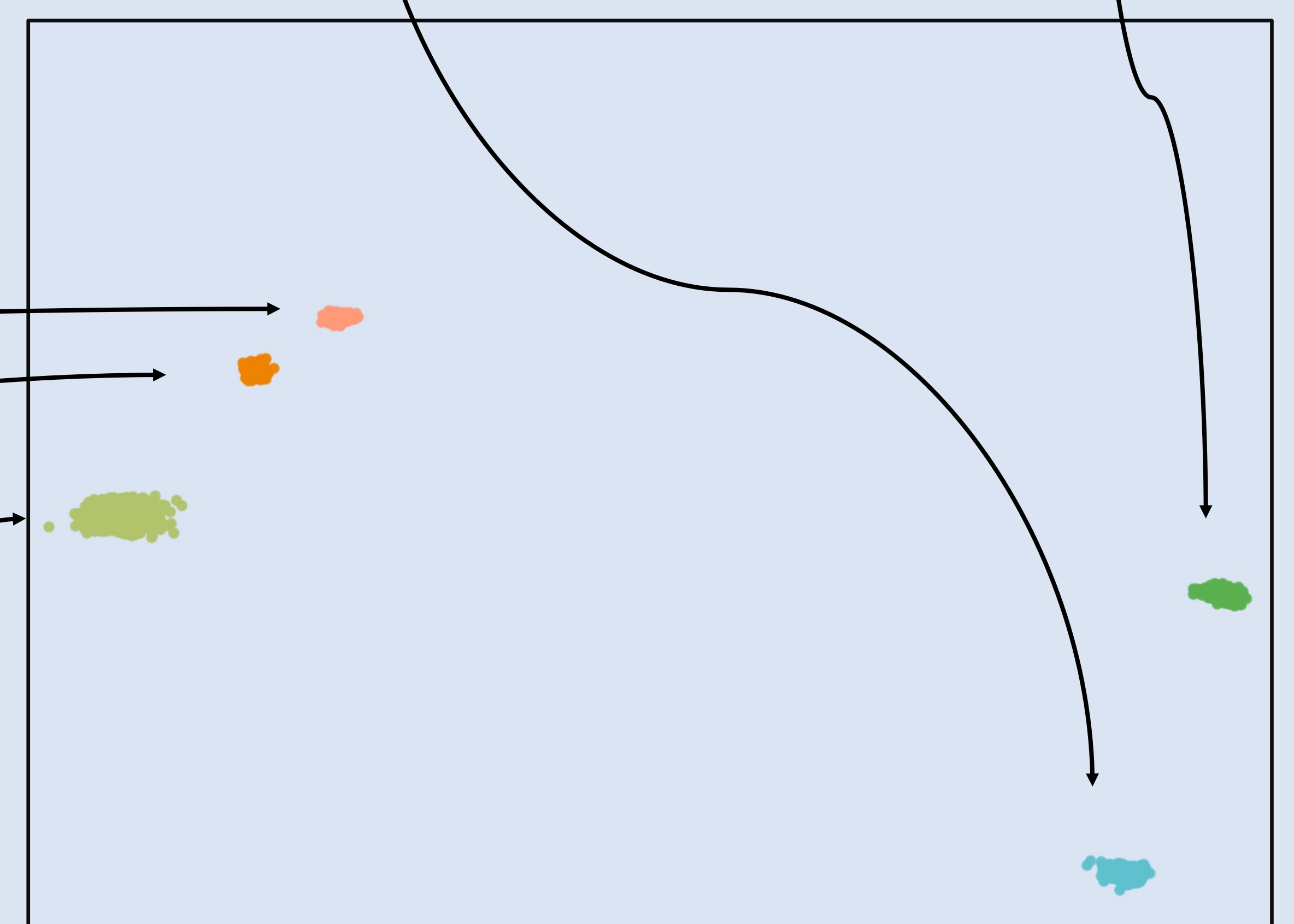
4. Age_{median} ≈ 40, little respiratory symptoms (, rhinitis)

5. Age_{median} ≈ 70, little respiratory symptoms, hypertension

1. Asthma, relatively few symptoms, family history of asthma/allergy

2. Asthma (diagnosed late), recurrent wheeze, nightly symptoms

3. Respiratory symptoms from exercise/tobacco smoke, fatigue



Conclusion

Clustering of self-reported respiratory symptoms has potential, but involves challenges for identifying novel phenotypes. Further optimization of embedding and clustering models is needed to improve robustness and resolution in clustering.

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